Pyruvate Oxidase Influences the Sugar Utilization Pattern and Capsule Production in Streptococcus pneumoniae

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Table S2 Genes with significantly lower expression profiles in *L. lactis* strain MG1363 suspended in KPi at pH 5.1, previously adapted to acid (grown at pH 5.1) compared with non-adapted cells (grown at 6.5).

Function	Gene	Fold change	Description of gene product
Amino acid transport and metabolism	dtpT	-2.6	di-/tripeptide transporter
	-	-2.3	putative amino-acid permease
	aroH	-2.7	phospho-2-dehydro-3-deoxyheptonate aldolase
	carA *	-2.6	carbamoyl phosphate synthase small subunit
	carB *	-2.6	carbamoyl phosphate synthase large subunit
	pabA *	-2.0	p-aminobenzoate synthetase, component II
Nucleotide transport and metabolism	tdk	-2.2	thymidine kinase
	purC	-2.5	phosphoribosylaminoimidazole-succinocarboxamide synthase
	purS	-2.5	phosphoribosylformylglycinamidine synthetase PurS
	purQ	-2.7	phosphoribosylformylglycinamidine synthase I
	purL	-2.5	phosphoribosylformylglycinamidine synthase II
	purM	-3.7	phosphoribosylaminoimidazole synthetase
	hprT	-2.0	HprT protein
	purH	-3.1	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
	purD	-2.3	phosphoribosylamine--glycine ligase
	purE	-2.2	phosphoribosylaminoimidazole carboxylase catalytic subunit
	pyrB	-3.0	aspartate carbamoyltransferase catalytic subunit
	pyrDB	-6.7	dihydroorotate dehydrogenase 1B
	pyrF	-3.3	orotidine 5'-phosphate decarboxylase
	mutT	-2.7	putative mutator protein
	pyrC	-2.1	dihydroorotase
	pyrE	-3.6	orotate phosphoribosyltransferase
	pbuX	-2.3	xanthine/uracil permease
	xpt	-4.1	xanthine phosphoribosyltransferase
	carA *	-2.6	carbamoyl phosphate synthase small subunit
	carB *	-2.6	carbamoyl phosphate synthase large subunit
Carbohydrate transport and metabolism	-	-2.0	sucrose-specific PTS enzyme IIABC
	-	-2.4	hypothetical protein llmg_1358
	dexC	-2.2	neopullulanase
	dexA	-2.6	oligo-1,6-alpha-glucosidase
Coenzyme transport and metabolism	hemH	-3.2	ferrochelatase
	thiD2	-2.2	phosphomethylpyrimidine kinase
	pabA *	-2.0	p-aminobenzoate synthetase, component II
Lipid transport and	accC	-2.1	acetyl-CoA carboxylase biotin carboxylase

Function	Gene	Fold change	Description of gene product
metabolism			subunit
	fabD	-2.9	malonyl CoA-acyl carrier protein transacylase
	-	-3.1	putative lysophospholipase
	-	-2.8	NAD(P)H dehydrogenase (quinone)
	mvk	-2.0	mevalonate kinase
	- *	-2.4	hypothetical protein llmg_1980
Translation	hemK	-2.	putative protoporphyrinogen oxidase
	truA	-2.1	tRNA pseudouridine synthase A
Transcription	lytR	-3.4	transcription regulator
	rlrG	-3.0	LysR family transcriptional regulator
	relA *	-2.3	GTP pyrophosphokinase
	llrE *	-2.0	two-component system regulator llrE
Replication, recombination and repair	ligA	-2.4	NAD-dependent DNA ligase LigA
	recJ	-2.2	single strand DNA-specific exonuclease
Cell wall/membrane biogenesis	-	-2.1	glycosyl transferase
	mreC	-2.1	cell shape determining protein mreC
Posttranslational modification, protein turnover, chaperones	trxB2	-3.0	TrxB2 protein
Inorganic ion transport and metabolism	kupB	-2.6	putative potassium transport system protein kupB
	phnD	-2.1	phosphonate ABC transporter, phosphonate-binding protein phnD
	phnC	-2.3	phosphonates import ATP-binding protein phnC
	phnB	-3.1	phosphonate transport system permease protein phnB
	-	-2.1	cation (calcium) transporting ATPase
	mntH	-2.0	putative proton-dependent manganese transporter group C beta
General function prediction only	-	-2.6	hypothetical protein llmg_2184
	-	-3.3	hypothetical protein llmg_1988
	pbuO	-3.0	xanthine/uracil/vitamin C permease
	-	-2.0	putative ABC transporter ATP-binding protein
	maa	-2.2	maltose O-acetyltransferase
	pabC	-2.6	putative aminodeoxychorismate lyase
	-	-2.0	hypothetical protein llmg_0332
	- *	-2.4	hypothetical protein llmg_1980
Function unknown	-	-2.3	hypothetical protein llmg_0377
	-	-2.4	hypothetical protein llmg_1024
	-	-2.1	hypothetical protein llmg_1025
	-	-2.1	hypothetical protein llmg_1760
	-	-2.1	hypothetical protein llmg_1941

Function	Gene	Fold change	Description of gene product
Signal transduction mechanisms	pppL	-2.4	putative phosphoprotein phosphatase
	ptpL	-2.4	protein-tyrosine phosphatase
	relA *	-2.3	GTP pyrophosphokinase
	llrE *	-2.0	two-component system regulator llrE
Intracellular trafficking and secretion	secY	-2.1	preprotein translocase subunit SecY
No prediction	rarA	-3.5	ArsR family transcriptional regulator
	-	-2.1	hypothetical protein llmg_1229
	-	-2.3	hypothetical protein llmg_1230
	-	-2.6	hypothetical protein llmg_2335
	-	-2.1	hypothetical protein llmg_2465